

Notch(C)	IDEĒ-SNP	QNGGTĒ---	D-VGSY-Ē-ĒPPGFT	ĒK---ĒE-N
10244(C)	-NEĒTM---	QQH---Ē	VNT-ĒSY-ĒKĒ-SĒ--	Ē--L-Ē D
80			ĒRĒFPĒYT	ĒKT ĒSQ D
95	VNEĒGMKPRP	ĒQHR Ē	VNTHĒSYKĒFĒLS	ĒHMLMP D
133	VNSRTCAMIN	ĒQYS Ē	EDTEĒGPQĒĒĒPSS	ĒLRĒAPN
175	IDEĒASGKVI	ĒPYNRĒĒ	VNTEĒSYĒKĒĒHĒFE	LQYISGR
220	INEĒTMSHT	ĒSHANĒ	FNTEĒGSF ĒKĒKQĒYK	ĒNGRLĒS
QDZIC)	V-ĒĒ-SG-Q--Ē-SS--Ē		-NTVĒSY-ĒRĒRĒĒW-P-PĒ-PN---	D
EGF(C)	NSDSEĒPLSHDGYĒLHDGVĒMYIEALDKYĒĒVĒVYI---		ĒER--ĒQYRDLKWWELR	

Figure 1

09981649-101501

GGCTGGAGAA GAAACAGCAA GGGAGTCTGT GAAGCTACAT GCGAACTGG  
ATGTAAGTTT GGTGAGTGG TGGGACCAA CAAATGCAGA TGCTTTCCAG  
GATACACCGG GAAAACCTGC AGTCAAGATG TGAATGAGTG TGGAAAGAAA  
CCCCGGCCAT GCCAACACAG ATGTGTGAAT ACACACGGAA GCTACAAGTG  
CTTTTGCTC AGTGGCCACA TGCTCATGCC AGATGCTACG TGTGTGAAGT  
CNAGGACATG TGCCATGATA AACTGTCAGT ATAGCTGTGA AGACACAGAA  
(SEQ ID NO 1)

GGCTGGAGAA GAAACAGCAA GGGAGTCTGT GAAGCTACAT GCGAACCTGG  
ATGTAAGTTT GGTGAGTGG TGGGACCAA CAAATGCAGA TGCTTTCCAG  
GATACACCGG GAAAACCTGC AGTCAAGATG TGAATGAGTG TGGAAAGAAA  
CCCCGGCCAT GCCAACACAG ATGTGTGAAT ACACACGGAA GCTACAAGTG  
CTTTTGCTC AGTGGCCACA TGCTCATGCC AGATGCTACG TGTGTGAAGT  
CNAGGACATG TGCCATGATA AACTGTCAGT ATAGCTGTGA AGACACAGAA  
GAAGGGCCAC AGTGCCTGTG TCCATCCTCA GGAATCCGCC TGGCCCCAAA  
TGAAGAGAC TGCTAGATA TTGATGAATG TGCCTCTGGT AAAGTCATCT  
GTCCCTACAA TCGAAGATGT GTGAACACAT TTGGAAGCTA CTAAGTCAAA  
TGTCACATTG GTTTCGAAGT GCAATATATC AGTGGACGAT ATGACTGTAT  
AGATATAAAT GAATGTACTA TGGATAGCCA TACGTGCAGC CACCATGCCA  
ATTGCTTCAA TACCCAAGGG TCCTTCAAGT GTAAATGCAA GCAGGGATAT  
AAAGGCAATG GACTTCGGTG TTCTGCTATC CCTGAAAATT CTGTGAAGGA  
AGTCCTCAGA GCACCTGGTA CCATCAAAGA CAGAATCAAG AAGTTGCTTG  
CTCACAAAAA CAGCATGAAA AAGAAGGCAA AAATTAAAAA TGTTACCCCA  
GAACCCACCA GGAATCCTAC CCCTAAGGTG AACTTGCAGC CCTTCAACTA  
TGAAGAGATA GTTTCAGAG GCGGGAATC TCATGGAGGT AAAAAAGGGA  
ATGAAGAGAA AATGAAAGAG GGGCTTGAGG ATGAGAAAAG AGAAGAGAAA  
GCCCTGAAGA ATGACATAGA GGAGCGAAGC CTGCGAGGAG ATGTGTTTTT  
CCCTAAGGTG AATGAAGCAG GTGAATTCGG CCTGATTCTG GTCCAAAGGA  
AAGCGCTAAC TTCCAAACTG GAACATAAAG ATTTAAATAT CTCGGTGGAC  
TGCAGCTTCA ATCATGGGAT CTGTGACTGG AAACAGGATA GAGAAGATGA  
TTTTGACTGG AATCCTGCTG ATCGAGATAA TGCTATTGGC TTCTATATGG  
CAGTTCGGGC CTTGGCAGGT CACATGAAAG ACATTGGCCG ATTGAAACTT  
CTCTACCTG ACCTGCAACC CCAAAGCAAC TTCTGTTTGC TCTTTGATTA  
CCGGCTGGCC GGAGACAAAAG TCGGGAAACT TCGAGTGTTT GTGAAAAACA  
GTAACAATGC CCTGGCATGG GAGAAGACCA CGAGTGAGGA TGAAAAGTGG  
AAGACAGGGA AAATTCAGTT GTATCAAGGA ACTGATGCTA CCAAAAGCAT  
CATTTTGA GACAGAACGTG GCAAGGGCAA AACCGGCGAA ATCGCAGTGG  
ATGGCGTCTT GCTTGTTC GGCCTATGTC CAGATAGCCT TTTATCTGTG  
GANNCTGAA TGGTACTATC TTTATATTTG ACTTTGTATG TCAGTTCCCT  
GGTTTTTTT ATATTGCATC ATAGGACCTC TGGCATTITA AAATTACTAG  
CTGAAAAATT G  
(SEQ ID NO 2)

Figure 2

GWRRNSKGVCEATCEPGCKFGECVGPNNKCRCPGYTGKTCSQDVNECGMKPRPCQHR  
CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTE  
(SEQ ID NO 3)

GWRRNSKGVCEATCEPGCKFGECVGPNNKCRCPGYTGKTCSQDVNECGMKPRPCQHR  
CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAP  
NGRDCLDIDECASGKVICPYNRRCVNTFGSYCKCHIGFELQYISGRYDCIDINECTMDS  
HTCSHHANCFNTQGSFKCKCKQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAH  
KNSMKKKAKIKNVTPEPTRTPPKVNLQPFNYEEIVSRGGNSHGKKGNEEKMKEGLE  
DEKREEKALKNDIEERSLRGDVFFPKVNEAGEFGLILVQRKALTSKLEHKDLNISVDCSF  
NHGICDWKQDREDDFDWNPADRDNAIGFYMAVPALAGHMKDIGRLKLLLPDLQPQSN  
FCLLFDYRLAGDKVGKLRVFKNSNNALAWEKTTSEDEKWKTGKIQLYQGTDATKSIIF  
EAERGKGKTGEIADVGVLLVSGLCPSLLSVDOXMVLSLYLTLVSSLVFLILHRTSGI  
LKLLAEKL  
(SEQ ID NO 4)

Figure 3

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Figure 4

ACTAGTGAATCCATCCTAATACGACTCACTATAGGGCTCGAGCGGCGCGCGGGCAGGTCTGCAGGGACAGCACCCGGTA  
ACTCCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGCGGCTTAGCTGCTACGGGGTCCGGCCGGCGCC  
CTCCCCAGGGGGGCTCAGGAGGAGGAAGGAGGACCCGTGCGAGAATGCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTG  
CTCCCCCTGGGTGGCAGGTGGTTTTCGGGAACCGCGCCAGTGCAGGCGATCACGGGTGTGTAGCATCGGCACGTCAGCCTGG  
GGTCTGTCACTATGGAATAAACTGGCCTGCTGCTACGGCTGGAGAAGAAAACAGCAAGGGAGTCTGTGAAGCTACATGCG  
AACCTGGATGTAAGTTTGGTGAAGTGCCTGGGACCAAAACAAATGCAGATGCTTTCCAGGATACACCGGGAAAACCTGCAGT  
CAAGATGTGAATGAGTGTGGAATGAAAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGGAAGCTACAAGTGCTT  
TTGCCCTCAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACTCTAGGACATGTGCCATGATAAACTGTCACTATA  
CTGTGTAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGACTCCGCCTGGCCCCAAATGGAAGAGACTGT  
CTAGATATTGATGAATGTGCCTCTGGTAAAGTCATCTGTCCCTACAATCGAAGATGTGTGAACACATTGGAAGCTACTA  
CTGCAATGTACATTGGTTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACTATGG  
ATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAAGGCTCCTTCAAGTGTAAATGCAAGCAGGGATATAAA  
GGCAATGGACTTCGGTGTCTGCTATCCCTGAAAATTCTGTGAAGGAAGTCTCAGAGCACCTGGTACCATCAAAGACAG  
AATCAAGAAGTTGCTTGCTCAAAAAACAGCATGAAAAAGAGGCAAAAAATTAATAATGTTACCCCAAGAACCCACAGGA  
CTCCTACCCCTAAGGTGAACCTTGCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAACTCTCATGGAGGTAAA  
AAAGGGAATGAAGAGAAAAATGAAGAGCGGGCTTGAGGATGAGAAAAGAGAAAGAGAAAGCCCTGAAGAAATGACWTAGAGGA  
GCGAAGCCTGCGAGGAGATGTGTTTTTCCCTAAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAG  
CGCTAACTTCCAACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACTGGAAA  
CAGGATAGAGAAAGATGATTTTGAAGTGAATCCTGCTGATCGAGATAATGCTATTGGCTTCTATATGGCAGTTCCGGCCCTT  
GGCAGGTCAAGAAAGACATTGGCCGATTGAACTTCTCCTACCTGACCTGCAACCCCAAGCAACTTCTGTTTGGCTCT  
TTGATTACCGGCTGGCCGGAGACAAAGTCCGGGAACTTCGAGTGTGTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAG  
AAGACCACGAGTGAAGGATGAAAAGTGAAGACAGGGAAATTCAGTTGTATCAAGGAAGTGTGCTACCAAAAGCATCAT  
TTTTGAAGCAGAACGTGGCCAGGGCAAAACCGCGGAAATCGCAGTGGATGGCGTCTTGCTTGTTCAGGCTTATGTCCAG  
ATAGCCTTTTATCTGTGGATGACTGAATGTTACTATCTTTATATTGACTTTGTATGTCAAGTTCCTGGTTTTTTTGATA  
TTGSATCATAGGACCTCTGGCATTTTAAAAATTACTAAGCTGAAAAATTGTAATGTACCAACAGAAATTATTATTGTAAGA  
TGCCTTTTMTGTATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCTTCTCAGTCAATTTCTGAATCTTTC  
CACATTATATTATAAAATATGGAATGTGAGGTTTATCTCCCTCCTCAGTATACCTGATTGTATAAGTAAGTTGATGA  
GCTTCTCTCTGCAACATTTCTAGAAAAATAGAAAAAAGCACAGAGAAATGTTTAACTGTTTGAAGTCTTATGATAGTTTT  
TGGAAACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAACTTGTATATTTAAAT  
TCTTTGTAATAATAATATCCAAATCATCAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO: 5)

Figure 5

MPLPWSLALPLLLPWVAGGFGNAAASARHHGLLASARQPGVCHYGTKLACCYGWRNRSKGVCEATCEPCKPGEQVGPNNKC  
RCFPGYTGKTCQSDVNECGMKPRPCQHRVCNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINQYSCEDTEBGPQCCLCP  
SGLRLAPNGRDCLDIDECASGKVICPYNARCNTFGSYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQ  
GSFKCKCKQYKGNGLRCSAIPENSVEVLRAFGTIKDRICKLLAHKNSMKKXAKIKNVTPETRTPTPKVNLQPFNYEE  
IVSRGGNSHGGKKGNEEKKKEGLEDEKREKALKNDXEERSLRGDVFFPKVNEAGEFGLILVQRKALTSKLEHKDLNISV  
DCSPNHGICDWKQDREDDFDWNFPADRDNAIGFYMAVPALAGHKDIGRLKLLLPDLQPQSNFCLLPDYRLAGDKVGKLRV  
FVKNSNNALAWKTTSEDEKWKTKGIQLYQGTDAKSIIFEAERKKGKTGEIAVDGVLLVSGLCPLDLSLVDD  
(SEQ ID NO: 6)

**EGFL6 (221-260 aa)**  
**3D Model**

**EGF**  
**NMR Structure**

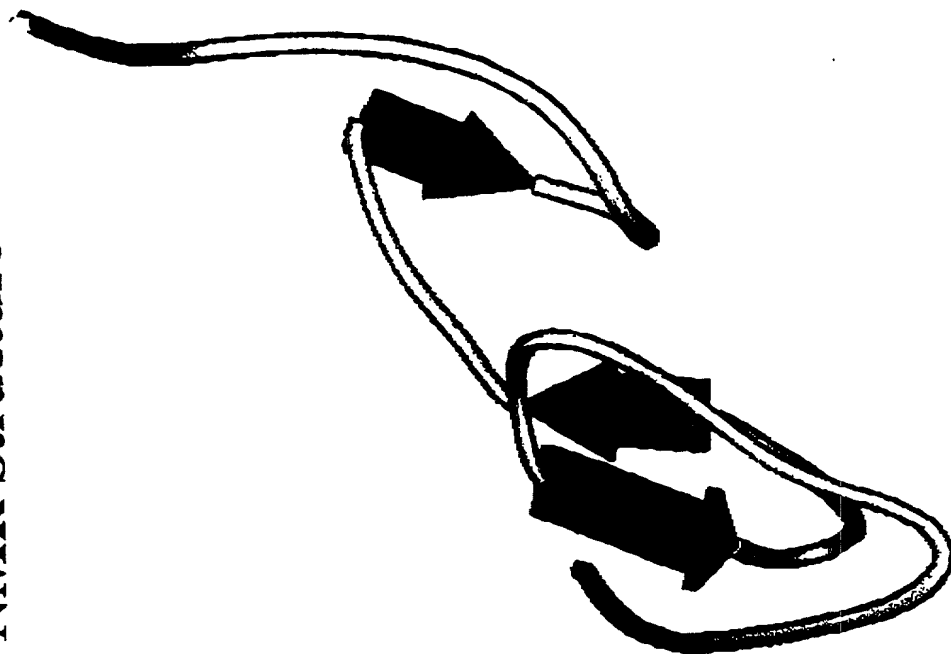
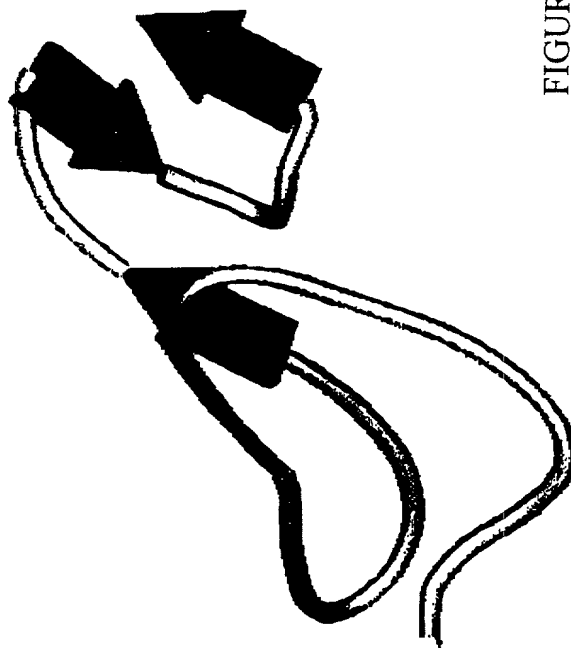


FIGURE 6